```
CGCTATCCCTCCCTCGTACAAACAAACGCAAGAGCAGCAATGGCCGTCCAGAAGTACACG   60
                                         M  A  V  Q  K  Y  T
                                        -25            -20
GTGGCTCTATTCCTCGCCGTGGCCCTCGTGGCGGGCCCGGCCGCCTCCTACGCCGCTGAC  120
 V  A  L  F  L  A  V  A  L  V  A  G  P  A  A  S  Y  A  A  D
       -15            -10            -5             1
GCCGGCTACACCCCCGCAGCCGCGGCCACCCCGGCTACTCCTGCTGCCACCCCGGCTGCG  180
 A  G  Y  T  P  A  A  A  A  T  P  A  T  P  A  A  T  P  A  A
    5              10             15             20
GCTGGAGGGAAGGCGACGACCGACGAGCAGAAGCTGCTGGAGGACGTCAACGCTGGCTTC  240
 A  G  G  K  A  T  T  D  E  Q  K  L  L  E  D  V  N  A  G  F
    25             30             35             40
AAGGCAGCCGTGGCCGCCGCTGCCAACGCCCCTCCGGCGGACAAGTTCAAGATCTTCGAG  300
 K  A  A  V  A  A  A  A  N  A  P  P  A  D  K  F  K  I  F  E
    45             50             55             60
GCCGCCTTCTCCGAGTCCTCCAAGGGCCTCCTCGCCACCTCCGCCGCCAAGGCACCCGGC  360
 A  A  F  S  E  S  S  K  G  L  L  A  T  S  A  A  K  A  P  G
    65             70             75             80
CTCATCCCCAAGCTCGACACCGCCTACGACGTCGCCTACAAGGCCGCCGAGGGCGCCACC  420
 L  I  P  K  L  D  T  A  Y  D  V  A  Y  K  A  A  E  G  A  T
    85             90             95             100
CCCGAGGCCAAGTACGACGCCTTCGTCACTGCCCTCACCGAAGCGCTCCGCGTCATCGCC  480
 P  E  A  K  Y  D  A  F  V  T  A  L  T  E  A  L  R  V  I  A
    105            110            115            120
GGCGCCCTCGAGGTCCACGCCGTCAAGCCCGCCACCGAGGAGGTCCCTGCTGCTAAGATC  540
 G  A  L  E  V  H  A  V  K  P  A  T  E  E  V  P  A  A  K  I
    125            130            135            140
```

Fig. 1

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```
CCACCGGTGAGCTGCAGATCGTTGACAAGATCGATGCTGCCTTCAAGATCGCAGCCACC   600
P  T  G  E  L  Q  I  V  D  K  I  D  A  A  F  K  I  A  A  T
   145            150            155            160
CCGCCAACGCCGCCCCCACCAACGATAAGTTCACCGTCTTCGAGAGTGCCTTCAACAAG   660
A  A  N  A  A  P  T  N  D  K  F  T  V  F  E  S  A  F  N  K
   165            170            175            180
CCCTCAATGAGTGCACGGGCGGCGCCTATGAGACCTACAAGTTCATCCCCTCCCTCGAG   720
A  L  N  E  C  T  G  G  A  Y  E  T  Y  K  F  I  P  S  L  E
   185            190            195            200
CCGCGGTCAAGCAGGCCTACGCCGCCACCGTCGCCGCCGCGCCCGAGGTCAAGTACGCC   780
A  A  V  K  Q  A  Y  A  A  T  V  A  A  A  P  E  V  K  Y  A
   205            210            215            220
TCTTTGAGGCCGCGCTGACCAAGGCCATCACCGCCATGACCCAGGCACAGAAGGCCGGC   840
V  F  E  A  A  L  T  K  A  I  T  A  M  T  Q  A  Q  K  A  G
   225            230            235            240
AACCCGCTGCCGCCGCTGCCACAGGCGCCGCAACCGTTGCCACCGGCGCCGCAACCGCC   900
K  P  A  A  A  A  A  T  G  A  A  T  V  A  T  G  A  A  T  A
   245            250            255            260
CCGCCGGTGCTGCCACCGCCGCTGCTGGTGGCTACAAAGCCTGATCAGCTTGCTAATAT   960
A  A  G  A  A  T  A  A  A  G  G  Y  K  A  *
   265            270            275
CTACTGAACGTATGTATGTGCATGATCCGGGCGGCGAGTGGTTTTGTTGATAATTAATC  1020
TCGTTTTCGTTTCATGCAGCCGCGATCGAGAGGGCTTGCATGCTTGTAATAATTCAATA  1080
TTTTCATTTCTTTTTGAATCTGTAAATCCCCATGACAAGTAGTGGGATCAAGTCGGCAT  1140
TATCACCGTTGATGCGAGTTTAACGATGGGGAGTTTATCAAAGAATTTATTATTAAAAA  1200
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA                                1229
```

Fig. 1 cont.

LIX-1	ADAGYTXAAAATXATXAATX
LIX-1.1	ADAGYTPAAAATPATPAATP
LIX-2	ATXATXAATXAAAGGKATTD
LIX-2.1	ATPATPAATPAAAGGKATTD
LIX-3	AAAGGKATTDEQKLLEDVNA
LIX-4	EQKLLEDVNAGFKAAVAAAA
LIX-5	GFKAAVAAAANAPPADKFKI
LIX-6	NAPPADKFKIFEAAFSESSK
LIX-7	FEAAFSESSKGLLATSAAKA
LIX-8	GLLATSAAKAPGLIPKLDTA
LIX-9	PGLIPKLDTAYDVAYKAAEG
LIX-10	YDVAYKAAEGATPEAKYDAF
LIX-11	ATPEAKYDAFVTALTEALRV
LIX-12	VTALTEALRVIAGALEVHAV
LIX-13	IAGALEVHAVKPATEEVPAA
LIX-14	KPATEEVPAAKIPTGELQIV
LIX-15	KIPTGELQIVDKIDAAFKIA
LIX-16	DKIDAAFKIAATAANAAPTN
LIX-17	ATAANAAPTNDKFTVFESAF
LIX-18	DKFTVFESAFNKALNECTGG
LIX-19	NKALNECTGGAYETYKFIPS
LIX-20	AYETYKFIPSLEAAVKQAYA
LIX-21	LEAAVKQAYAATVAAAPEVK
LIX-22	ATVAAAPEVKYAVFEAALTK
LIX-23	YAVFEAALTKAITAMTQAQK
LIX-24	AITAMTQAQKAGKPAAAAAT
LIX-25	AGKPAAAAATGAATVATGAA
LIX-26	GAATVATGAATAAAGAATAA
LIX-27	TAAAGAATAAAGGYKA

X REPRESENTS HYDROXYPROLINE RESIDUE

Fig. 2

PEPTIDE NAME	PEPTIDE SEQUENCE
LPI-1	IAKVPPGPNITAEYGDKWLD
LPI-1.1	IAKVXPGXNITAEYGDKWLD
LPI-2	TAEYGDKWLDAKSTWYGKPT
LPI-3	AKSTWYGKPTGAGPKDNGGA
LPI-4	GAGPKDNGGACGYKNVDKAP
LPI-4.1	GAGPKDNGGACGYKDVDKAP
LPI-5	CGYKDVDKAPFNGMTGCGNT
LPI-6	FNGMTGCGNTPIFKDGRGCG
LPI-7	PIFKDGRGCGSCFEIKCTKP
LPI-8	SCFEIKCTKPESCSGEAVTV
LPI-9	ESCSGEAVTVTITDDNEEPI
LPI-10	TITDDNEEPIAPYHFDLSGH
LPI-11	APYHFDLSGHAFGSMADDGE
LPI-11.1	APYHFDLSGHAFGSMAKKGE
LPI-12	AFGSMADDGEEQKLRSAGEL
LPI-12.1	AFGSMAKKGEEQKLRSAGEL
LPI-13	EQKLRSAGELELQFRRVKCK
LPI-14	ELQFRRVKCKYPDDTKPTFH
LPI-15	YPDDTKPTFHVEKASNPNYL
LPI-16	VEKASNPNYLAILVKYVDGD
LPI-16.1	VEKGSNPNYLAILVKYVDGD
LPI-17	AILVKYVDGDGDVVAVDIKE
LPI-18	GDVVAVDIKEKGKDKWIELK
LPI-19	KGKDKWIELKESWGAVWRID
LPI-20	ESWGAVWRIDTPDKLTGPFT
LPI-21	TPDKLTGPFTVRYTTEGGTK
LPI-22	VRYTTEGGTKSEVEDVIPEG
LPI-23	SEVEDVIPEGWKADTSYSAK

Fig. 3

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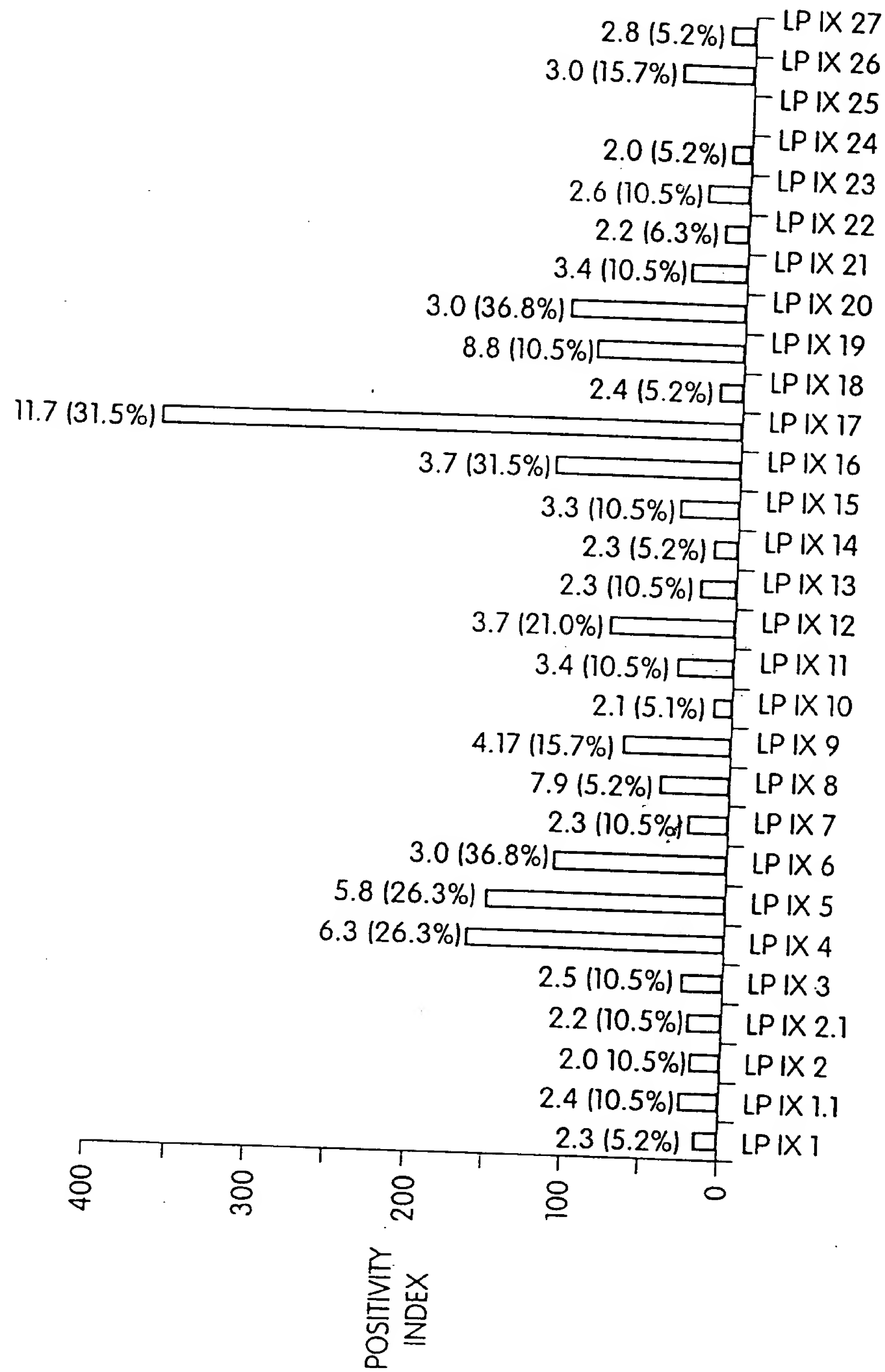


Fig. 4

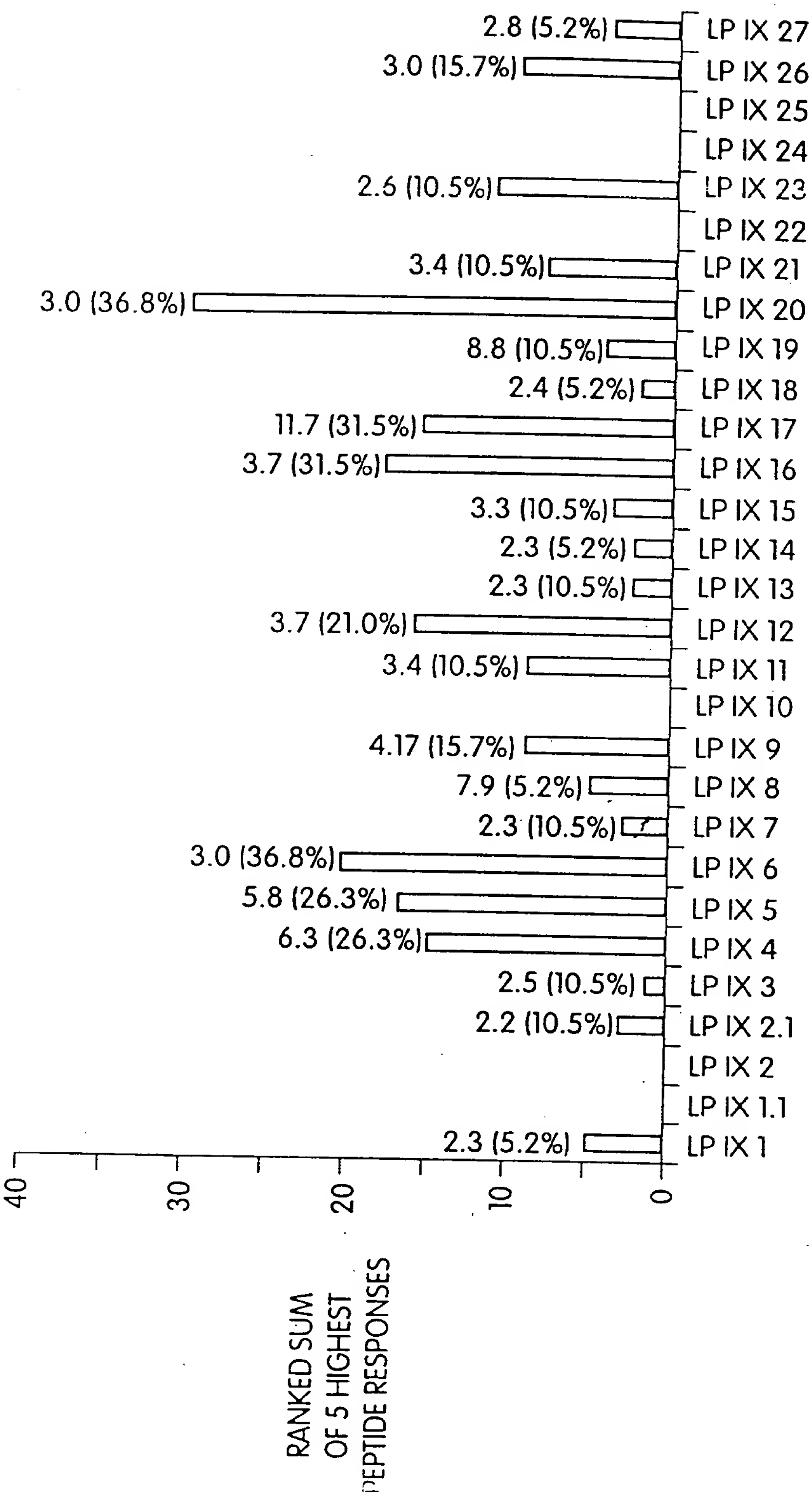

2.8 (5.2%)
3.0 (15.7%)
2.6 (10.5%)
3.4 (10.5%)
3.0 (36.8%)
8.8 (10.5%)
2.4 (5.2%)
11.7 (31.5%)
3.7 (31.5%)
3.3 (10.5%)
2.3 (5.2%)
2.3 (10.5%)
3.7 (21.0%)
3.4 (10.5%)
4.17 (15.7%)
7.9 (5.2%)
2.3 (10.5%)
3.0 (36.8%)
5.8 (26.3%)
6.3 (26.3%)
2.5 (10.5%)
2.2 (10.5%)
2.3 (5.2%)
LP IX 27
LP IX 26
LP IX 25
LP IX 24
LP IX 23
LP IX 22
LP IX 21
LP IX 20
LP IX 19
LP IX 18
LP IX 17
LP IX 16
LP IX 15
LP IX 14
LP IX 13
LP IX 12
LP IX 11
LP IX 10
LP IX 9
LP IX 8
LP IX 7
LP IX 6
LP IX 5
LP IX 4
LP IX 3
LP IX 2.1
LP IX 2
LP IX 1.1
LP IX 1
40
30
20
10
0
RANKED SUM
OF 5 HIGHEST
PEPTIDE RESPONSES

Fig. 5

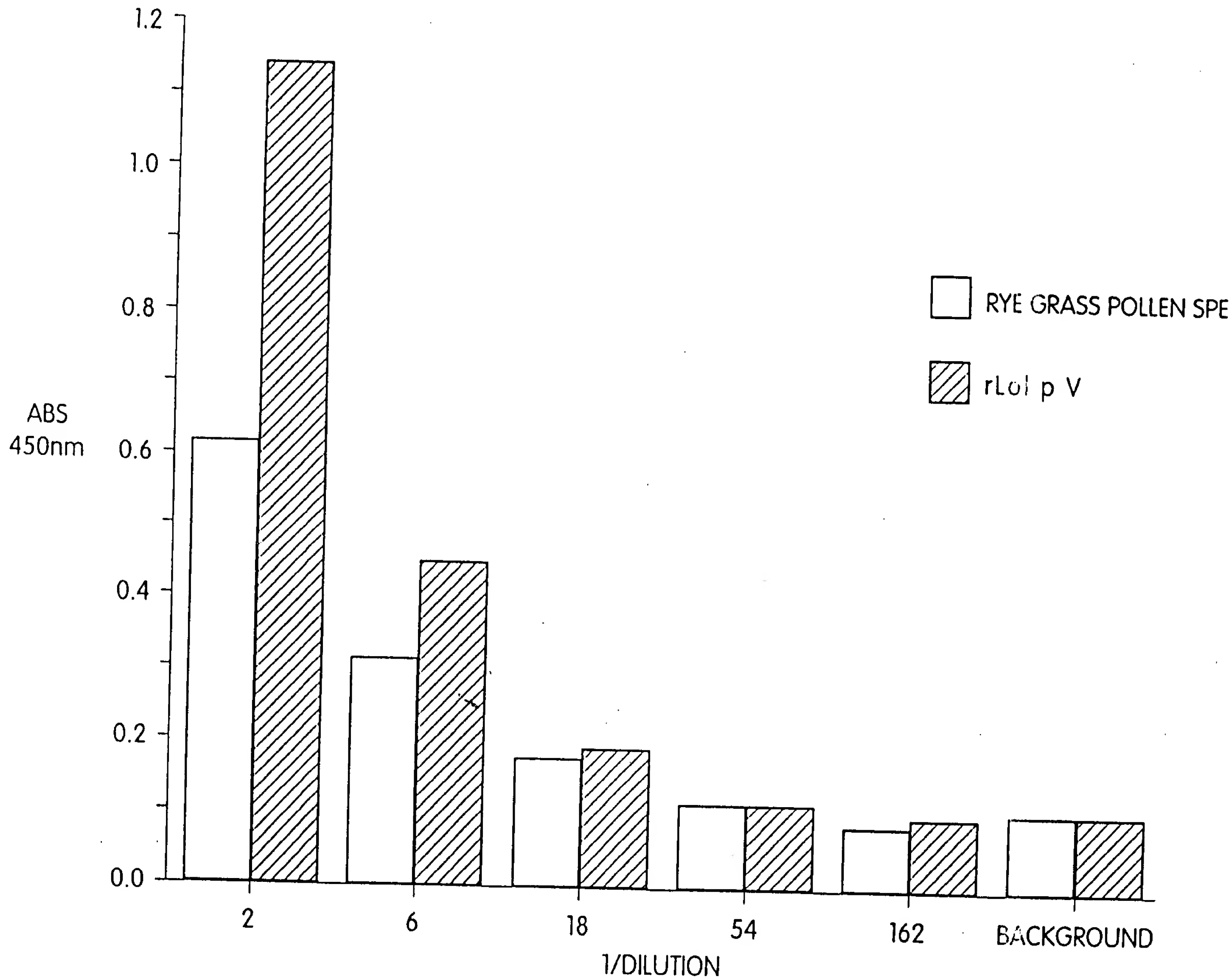

ABS
450nm
1.2
1.0
0.8
0.6
0.4
0.2
0.0
RYE GRASS POLLEN SPE
rLol p V
2
6
18
54
162
BACKGROUND
1/DILUTION

Fig. 6

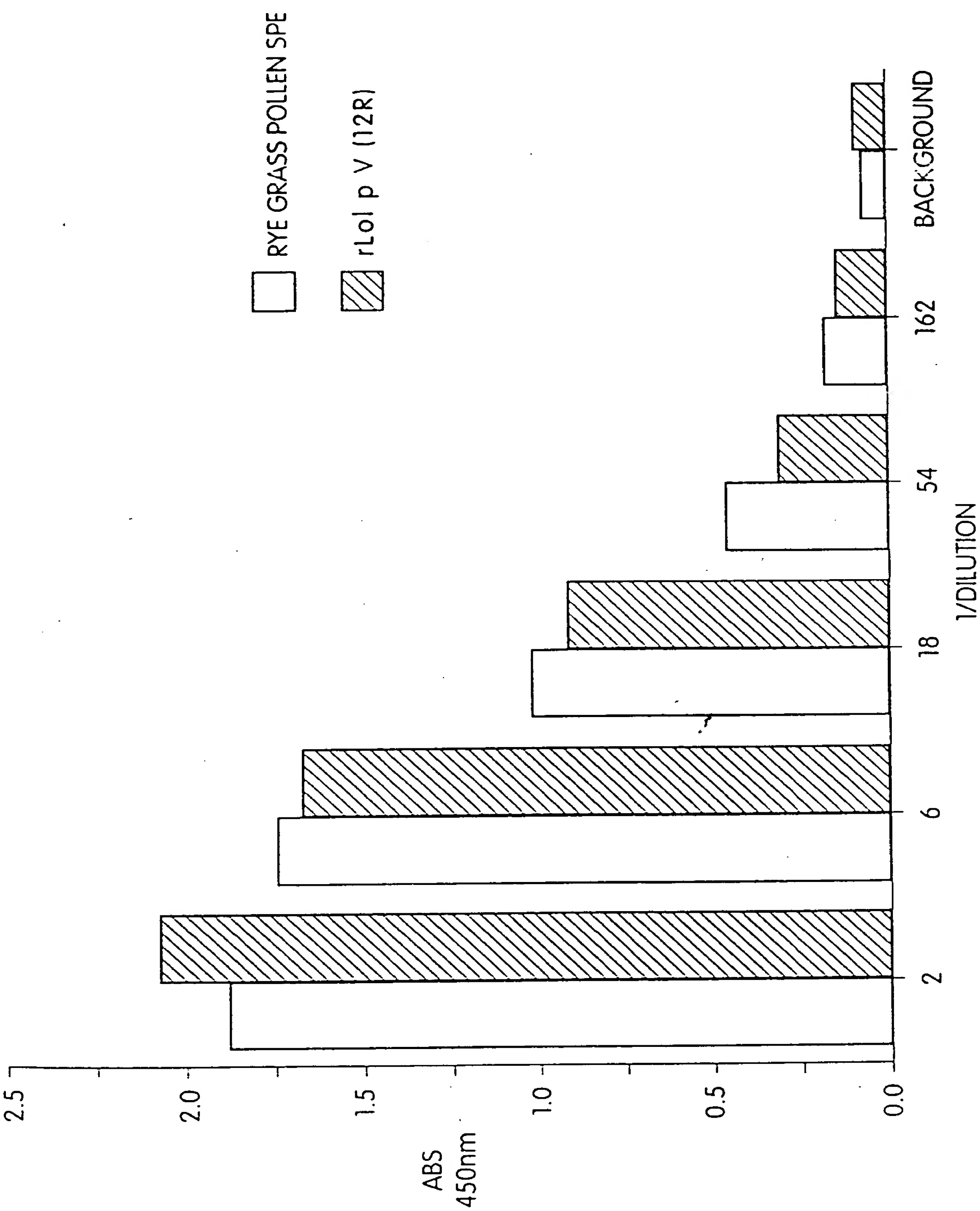

RYE GRASS POLLEN SPE
rLol p V (12R)
ABS
450nm
2.5
2.0
1.5
1.0
0.5
0.0
2
6
18
54
162
BACKGROUND
1/DILUTION

Fig. 7

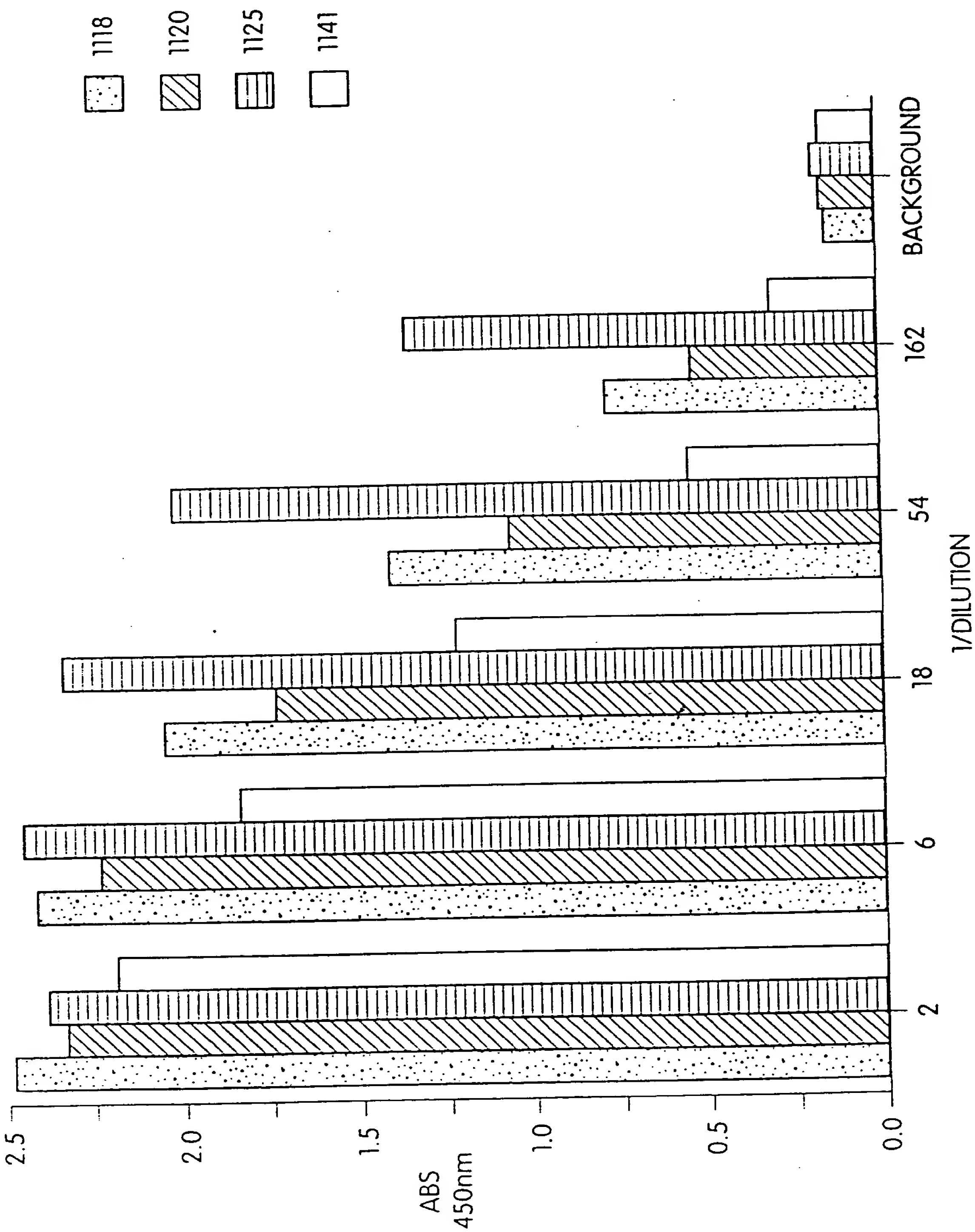
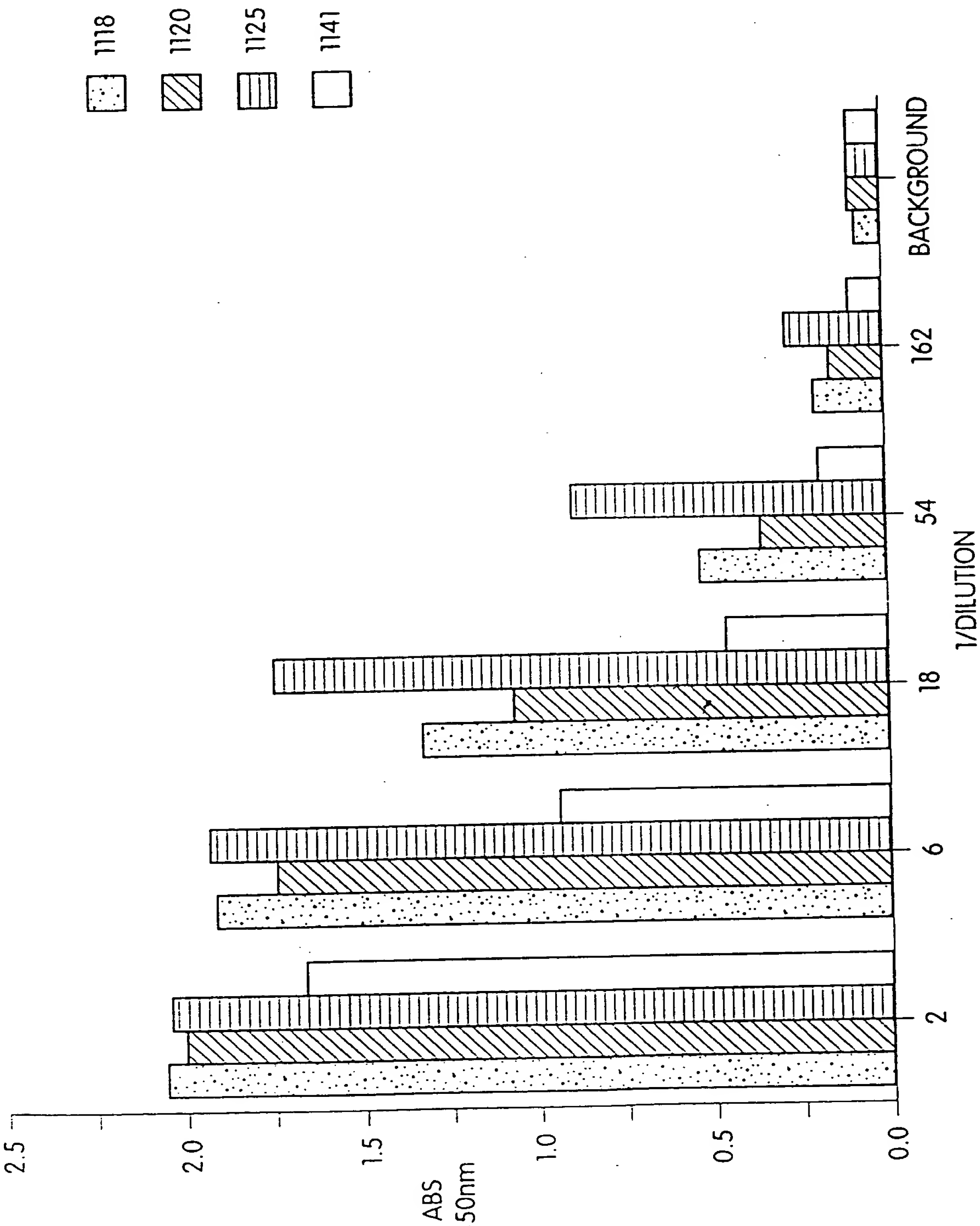

1118
1120
1125
1141
ABS 450nm
2.5
2.0
1.5
1.0
0.5
0.0
2
6
18
54
162
BACKGROUND
1/DILUTION

Fig. 8



1118
1120
1125
1141
ABS
450nm
2.5
2.0
1.5
1.0
0.5
0.0
2
6
18
54
162
BACKGROUND
1/DILUTION

Fig. 9

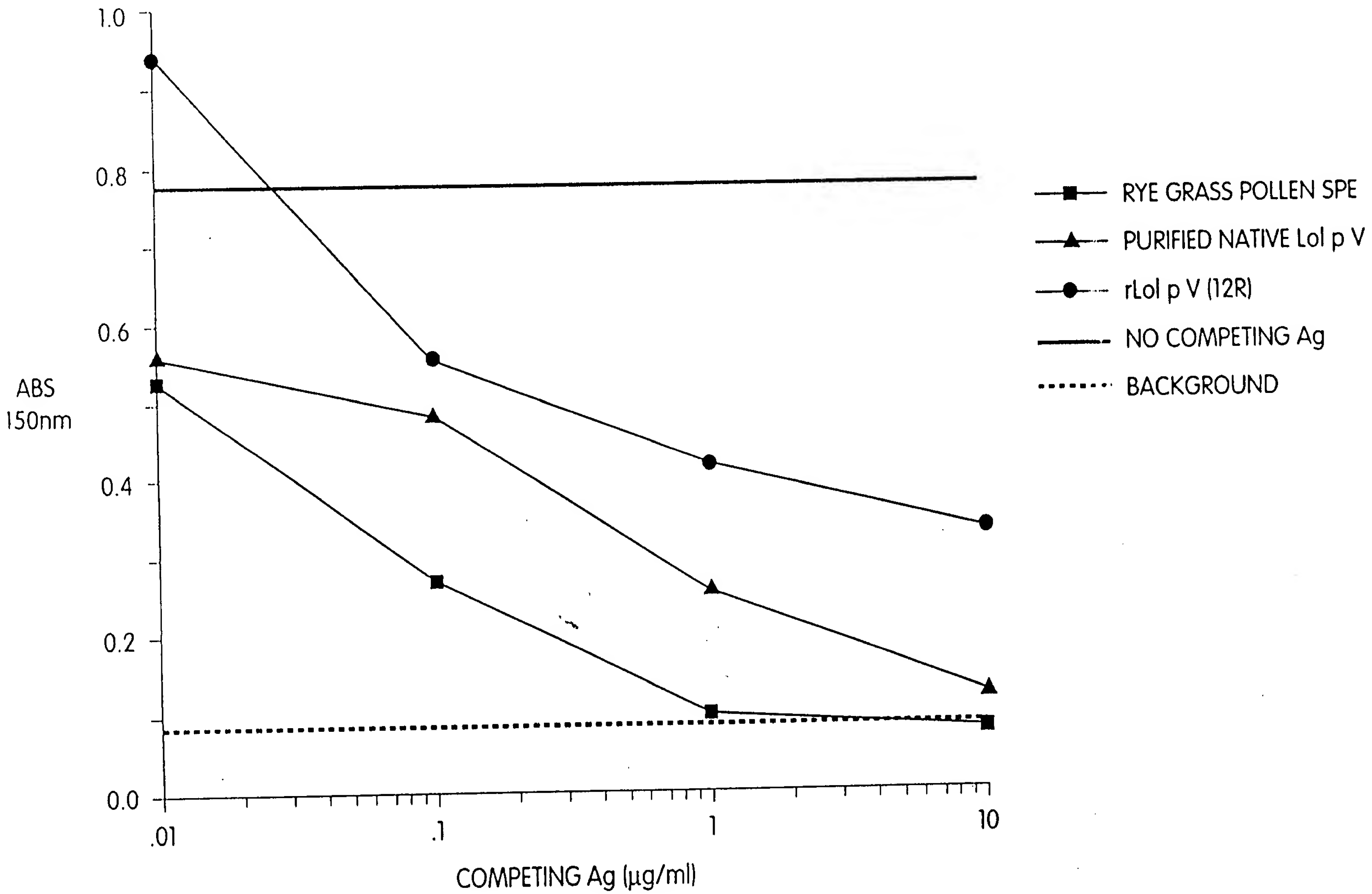
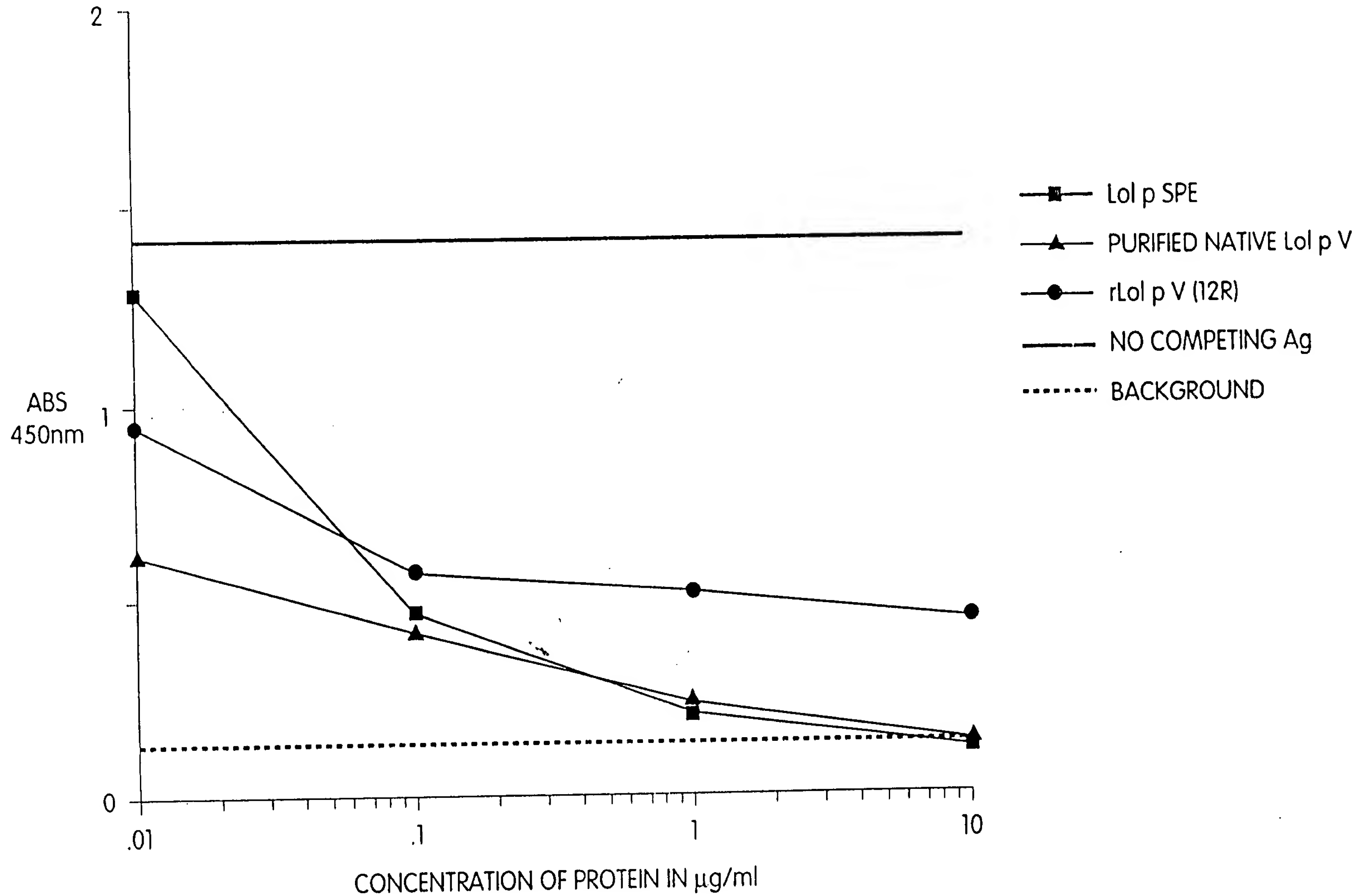
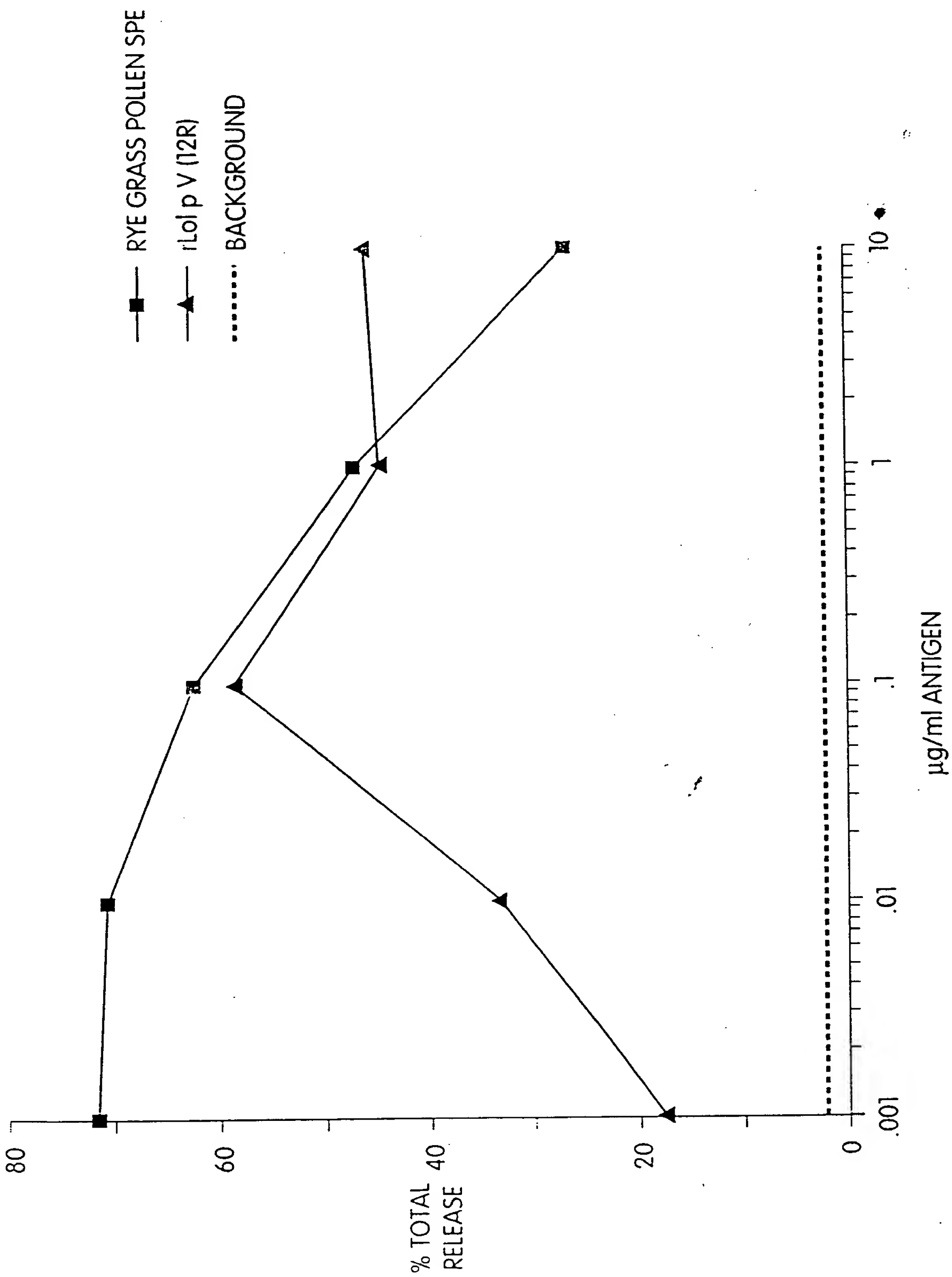

1.0
0.8
0.6
0.4
0.2
0.0
ABS
150nm
.01
.1
1
10
COMPETING Ag (µg/ml)
RYE GRASS POLLEN SPE
PURIFIED NATIVE Lol p V
rLol p V (12R)
NO COMPETING Ag
BACKGROUND

Fig. 10



2
1
0
ABS
450nm
.01
.1
1
10
CONCENTRATION OF PROTEIN IN µg/ml
Lol p SPE
PURIFIED NATIVE Lol p V
rLol p V (12R)
NO COMPETING Ag
BACKGROUND

Fig. 11



RYE GRASS POLLEN SPE
rLol p V (12R)
BACKGROUND
% TOTAL RELEASE
80
60
40
20
0
.001
.01
.1
1
10
µg/ml ANTIGEN

Fig. 12

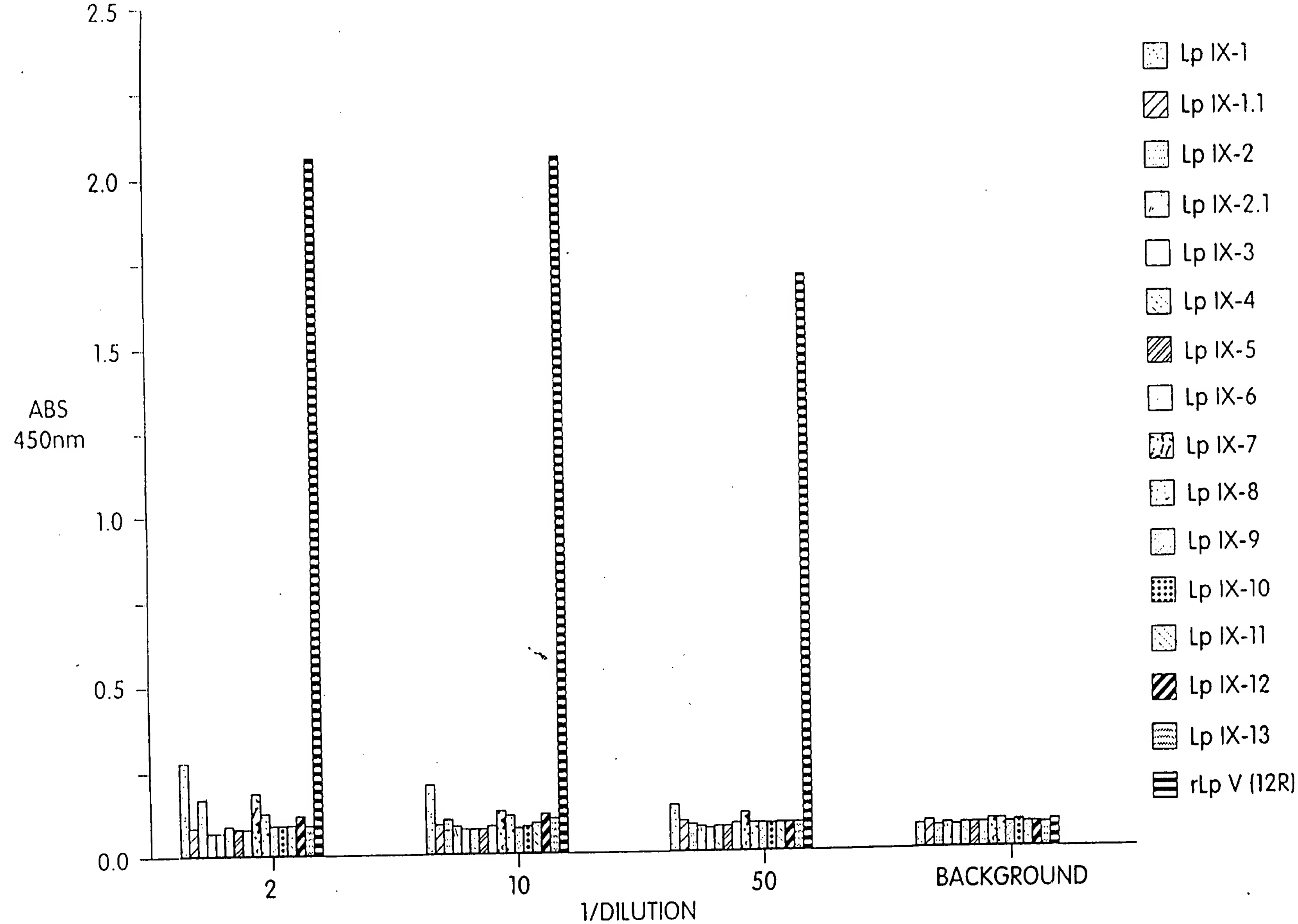
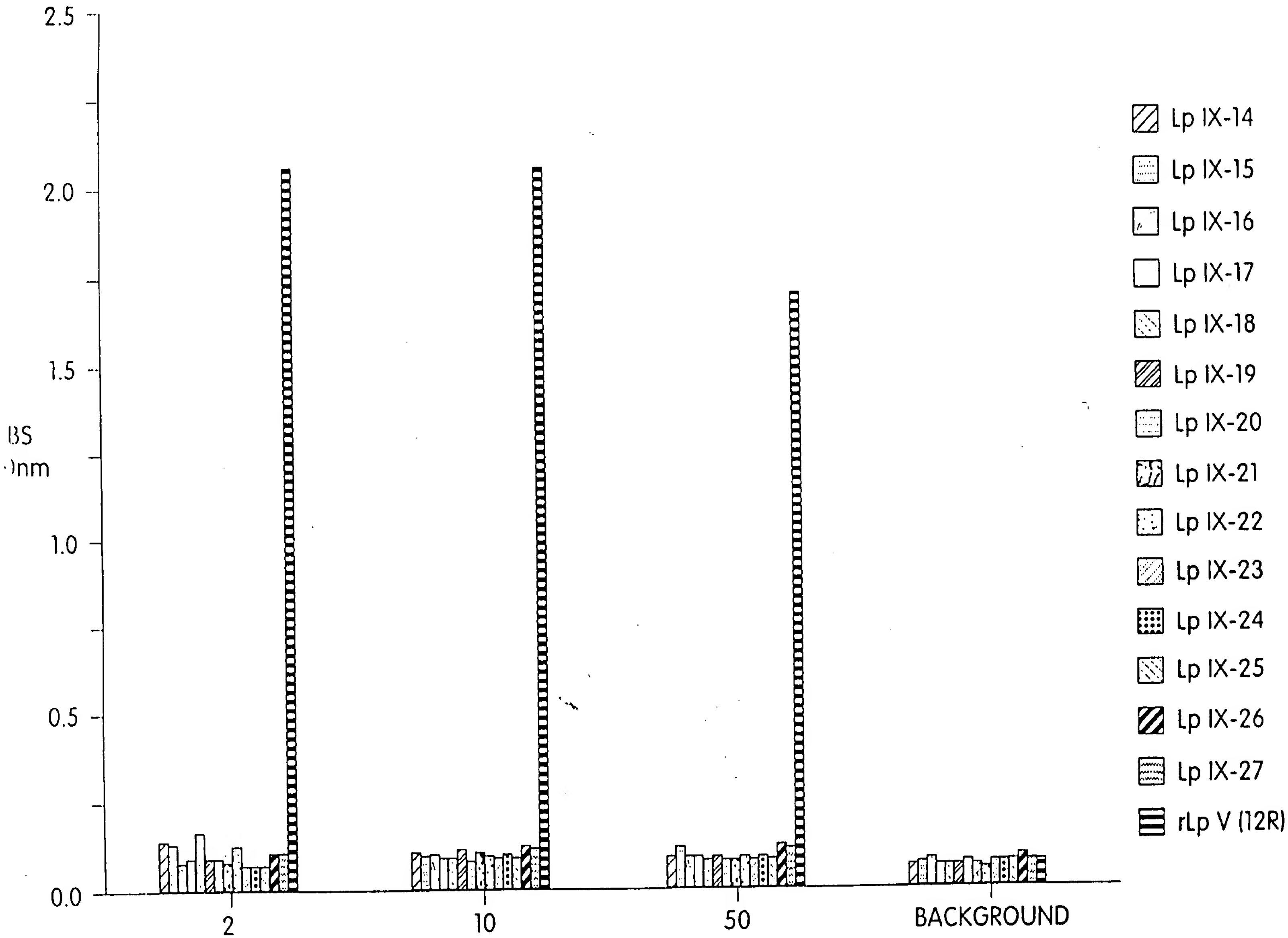

2.5
2.0
1.5
1.0
0.5
0.0
ABS
450nm
2
10
50
BACKGROUND
1/DILUTION
Lp IX-1
Lp IX-1.1
Lp IX-2
Lp IX-2.1
Lp IX-3
Lp IX-4
Lp IX-5
Lp IX-6
Lp IX-7
Lp IX-8
Lp IX-9
Lp IX-10
Lp IX-11
Lp IX-12
Lp IX-13
rLp V (12R)

Fig. 13A



2.5
2.0
1.5
1.0
0.5
0.0
BS
nm
2
10
50
BACKGROUND
1/DILUTION
Lp IX-14
Lp IX-15
Lp IX-16
Lp IX-17
Lp IX-18
Lp IX-19
Lp IX-20
Lp IX-21
Lp IX-22
Lp IX-23
Lp IX-24
Lp IX-25
Lp IX-26
Lp IX-27
rLp V (12R)

Fig. 13B

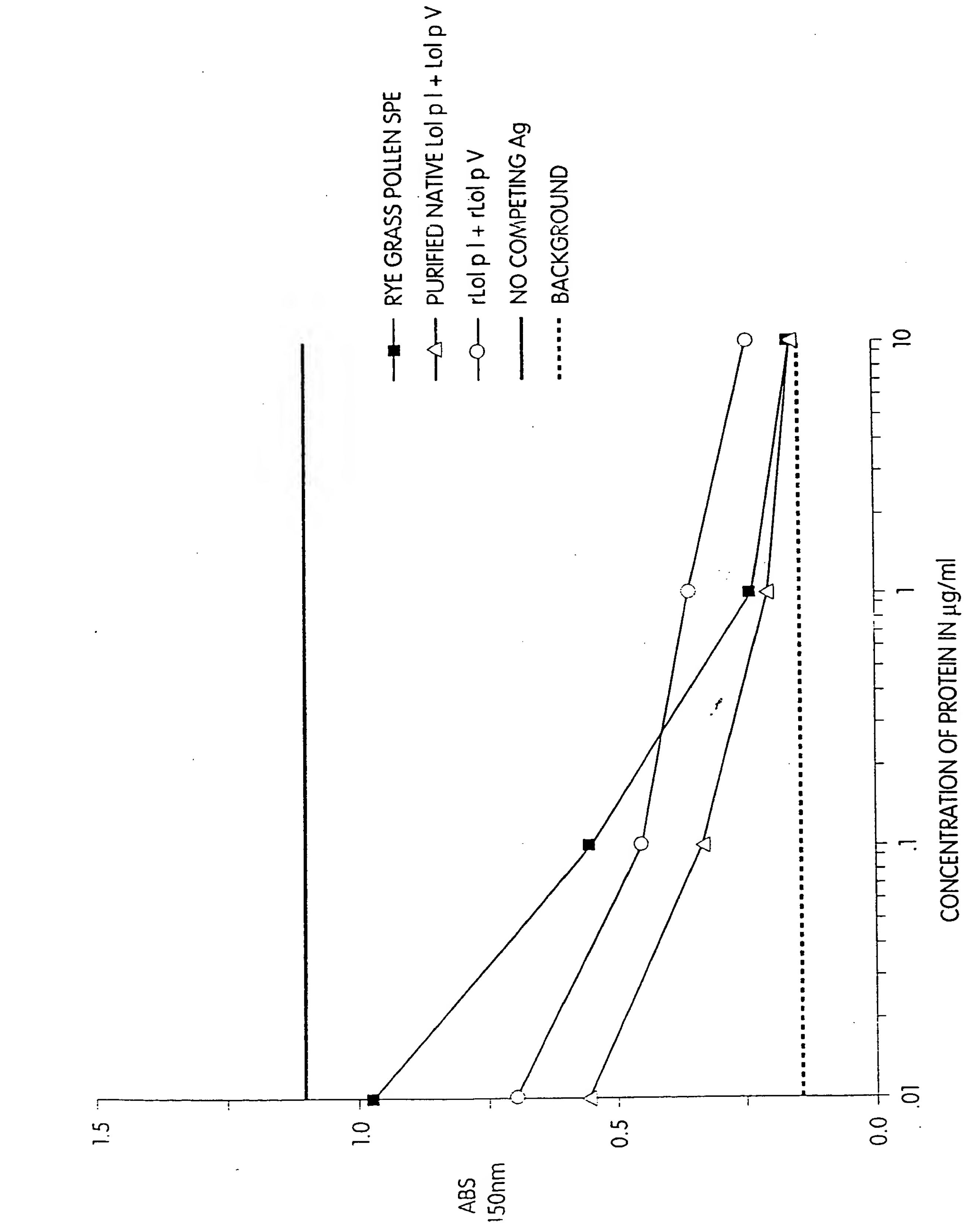

RYE GRASS POLLEN SPE
PURIFIED NATIVE Lol p I + Lol p V
rLol p I + rLol p V
NO COMPETING Ag
BACKGROUND
ABS
150nm
1.5
1.0
0.5
0.0
.01
.1
1
10
CONCENTRATION OF PROTEIN IN µg/ml

Fig. 14

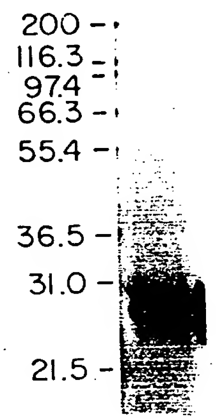


Fig. 15

```
GAATTCGAGGATCCGGGTACCATGGCTCCGACAAACCAACGCAAGAGCAGCAATGGCA  58
                                                       M  A
                                                      -24
GTGCAGCAGTACACGGTGGCGCTGTTCCTGGCCGTGGCCTCGTGTCGGGCCCGCGCCTCC  118
 V  Q  Q  Y  T  V  A  L  F  L  A  V  A  S  C  R  A  R  A  S
   -20                                   -10
TACGCCGCCGACGCCGGCTACGCCCCCGCCACTCCCGCCACCCCGGCTACCCCCGCGGCC  178
 Y  A  A  D  A  G  Y  A  P  A  T  P  A  T  P  A  T  P  A  A
       1                                  10
CCAGGCGCAGCGGTGCCAGCAGGGAAGGCGGCGACCGAGGAGCAGAAGCTGATCGAGAAG  238
 P  G  A  A  V  P  A  G  K  A  A  T  E  E  Q  K  L  I  E  K
   20                                     30
ATCAACGCCGGCTTCAAGGCCGCCGTGGCGGCCGCCGCGGGCGTCCCGCCAGGCGACAAG  298
 I  N  A  G  F  K  A  A  V  A  A  A  A  G  V  P  P  A  D  K
   40                                     50
TACAAGACGTTCGTCGAAACCTTCGGCAAGGCCTCCAACAAGGCCTTCCTGGGGGACCTC  358
 Y  K  T  F  V  E  T  F  G  K  A  S  N  K  A  F  L  G  D  L
   60                                     70
CCGACCAACTACGCCGATGTCAACTCCAGGGCCCAGCTCACCTCGAAGCTCGACGCCGCC  418
 P  T  N  Y  A  D  V  N  S  R  A  Q  L  T  S  K  L  D  A  A
   80                                     90
TACAAGCTCGCCTACGACGCCGCCCAGGGCGCCACCCCCGAGGCCAAGTACGACGCCTAC  478
 Y  K  L  A  Y  D  A  A  Q  G  A  T  P  E  A  K  Y  D  A  Y
  100                                    110
```

Fig. 16

```
TCGCCACCCTCAGCGAGGCGCTCCGCATCATCGCCGGCACCCTCGAGGTCCACGCCGTC  538
V  A  T  L  S  E  A  L  R  I  I  A  G  T  L  E  V  H  A  V
 120                                    130
AGCCCGCTGCCGAGGAGGTCAAGCCTATCCCCGCCGGAGAGCTGCAGATCGTCGACAAG  598
K  P  A  A  E  E  V  K  P  I  P  A  G  E  L  Q  I  V  D  K
 140                                    150
TTGACGTCGCCTTCAGAACTGCCGCCACCGCCGCCAACGCCGCCCCCACCAACGACAAG  658
I  D  V  A  F  R  T  A  A  T  A  A  N  A  A  P  T  N  D  K
 160                                    170
TCACCGTATTCGAGACCACCTTTAACAAGGCCATCAAGGAGAGCACGGGCGGCACCTAC  718
F  T  V  F  E  T  T  F  N  K  A  I  K  E  S  T  G  G  T  Y
 180                                    190
AGAGCTACAAGTTCATTCCCACCCTTGAGGCCGCCGTTAAGCAGGCCTACGCCGCCACC  778
E  S  Y  K  F  I  P  T  L  E  A  A  V  K  Q  A  Y  A  A  T
 200                                    210
TCGCATCCGCGCCGGAGGTCAAGTACGCCGTCTTTGAGACCGCGCTGAAAAAGGCGGTC  838
V  A  S  A  P  E  V  K  Y  A  V  F  E  T  A  L  K  K  A  V
 220                                    230
CCGCCATGTCCGAGGCCCAGAAGGAAGCCAAGCCCGCCACCGCCACCCCGACCCCCACC  898
T  A  M  S  E  A  Q  K  E  A  K  P  A  T  A  T  P  T  P  T
 240                                    250
```

Fig. 16 cont.

```
CAACTGCCGCGGCCGCGGTGGCCACCAACGCCGCCCCGTCGCTGCTGGTGGCTACAAA   958
A  T  A  A  A  A  V  A  T  N  A  A  P  V  A  A  G  G  Y  K
 260                        270
TCTGATCAACTCGCTAGCAATATACACATCCATCATGCACATATAGAGCTGTGTATGTA  1018
I  *
GTGCATGCATGCCGTGGCGCCGCGCAAGTTTGCTCATAATTAATTCTTGGTTTTCGTTG  1078
TTGCATCCACGAGCGACCGAGCCCGTGGATAGTCGCATGTGTATGTAATTTTTTCTGAG  1138
AATGTGTATATGTAATATATAATTGAGTACTAAAAAAAAAAA                   1181
```

Fig. 16 cont.